

Enhancing Cervical Cancer Diagnosis through Advanced Feature Engineering and Machine Learning Techniques

Farouk Sadi Ph.D¹, Associate Professor Mu'azu Musa Jibrin², Professor Abubakar Sadiq Haruna³, Engr. Mohammed Ibrahim Buhari⁴

¹ Kano State College of Nursing Sciences

E-mail: farouksadi2020@gmail.com

² Ahmadu Bello University

³ Federal University Gusau

⁴ Bradford University Graduate

E-mail: mohammedibrahimbuhari@yahoo.com

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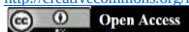
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ABSTRACT

Cervical cancer continues to be a considerable global health problem, with a burden disproportionately in the developing world, where it ranks as the fourth most common cancer among women. Although this disease is preventable with timely diagnosis and treatment, current modalities available for screening such as Pap smear and HPV testing are limited due to barriers in accessibility, cost, and variability in interpretation of results. This requires building up more powerful diagnostic tools. In recent years, machine learning (ML) and the feature engineering process, have opened the possibility of improving cervical cancer diagnosis by evaluating very deep patterns hidden in medical data and not perceived by human analysis. Also, different machine learning models like Logistic Regression, Random Forest, Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Decision Trees are the best for diagnostic purpose accuracy, precision, recall and F1-score after applying the feature selection techniques. Specifically, the findings highlight the value of more sophisticated feature engineering to augment the data representation and improve model outcomes, as evidenced by Logistic Regression and SVM's perfect F1 of 0.80 showing their clinical utility. It ends also with challenges, such as the need for large, annotated datasets and how to deal with the interpretability of complex models, as well as a set of actionable recommendations for improving diagnostics methodologies. The findings of this work highlight the role of machine learning in cervical cancer diagnosis and its potential to improve patient outcomes through early detection and prevention.

Introduction

Cervical cancer continues to pose a major global health challenge especially in developing countries where it is the fourth most prevalent cancer among women (World Health Organization [WHO], 2023). Although largely preventable through timely detection and treatment, up to 570,000 new cases and 311,000 deaths from gastric cancer were recorded worldwide in 2022 (Small et al., 2023). While the conventional screening techniques, which are primarily based on Papanicolaou (Pap) smear tests and human papillomavirus (HPV) testing, have proven effective, these methods face several challenges, including accessibility and cost, as well as varying test interpretations (Kumar et al., 2022). Screening techniques like Pap smear test and testing for HPV DNA play a major role in this, since the earlier a person is treated for cancer, which is now cure-able in its initial stages, the better the cases will be successfully addressed. Yet, conventional screening methods may face challenges such as interpretation variability, accessibility issues, and lack of follow-up care (Schiffman et al., 2011). Hence, the need for more robust diagnostic tools that improve accuracy and efficacy in cervical cancer detection.

Machine learning (ML) and feature engineering techniques have also been integrated into this framework in recent years, which have become an effective means of improving the accuracy and efficiency of cervical cancer diagnosis. These computational techniques have the capability to detect

intricate patterns in medical data that may be unnoticed by human observers, potentially facilitating earlier and more accurate diagnoses (Zhang & Chen, 2024). Novel region based features coupled with supervised learning techniques provides a potent synergy to boost the predictive performance in cervical cancer diagnosis. In this work we focus on machine learning models like Logistic Regression, Random Forest, Support Vector Machines (SVM), K-Nearest Neighbors (KNN), and Decision Trees, used in conjunction with correlation-based filtering methods for feature selection. This work also aims to create a comprehensive pipeline for diagnostic processing of cervical cancer by optimizing the performance metrics accuracy, precision, recall and F1-score.

Screening tests for cervical cancer have a long way since the Pap smear was introduced by George Papanicolaou in the 1940s and substantial developments occurred along the way towards the state of the art testing today. With the advent of digital pathology and automated screening systems, these technologies have made their way up the quality scale and allowed for more standardized, objective analyses (Thompson et al., 2023). Nevertheless, cervical cytology images are difficult to interpret, which can be attributed to overlapping cells, variable staining quality and the existence of inflammatory cells or debris (Liu et al., 2023). Among different aspects of machine learning applications, feature engineering is an important one, which determines the extraction and selection of such characteristics from medical data to effectively differentiate normal and abnormal indications of the cervical cells. These include morphometric features (nuclear size and shape), textural properties and spatial relations among cells (Rodriguez-Sanchez et al., 2023). However, TAE techniques have been shown to maintain capture of minor patterns and relationships in the imaging data which goes unnoticed in the standard EM algorithms with potential benefits including increased accuracy of automated screening systems based on the local findings represented by it.

Different machine learning techniques have been used in studies conducted for cervical cancer diagnosis, these include custom deep learning architectures, ensemble based methods, hybrid models etc. Recent advancements in Convolutional Neural Networks (CNNs) exhibit great potential in automatically extracting hierarchical features of cervical cytology images (Wang et al., 2023). Furthermore, merger of various data sources encompassing clinical history, molecular markers, and imaging data has resulted in the establishment of more robust and comprehensive diagnostic models (Chen et al., 2023). Although the above advances, there are still some challenges faced in practically implementing the ML-based diagnosis systems for cervical cancer. Such challenges include ensuring the availability of large-scale, well-annotated datasets for training purposes, ensuring interpretability of complex models, and validating these systems in heterogeneous patient populations and clinical settings (Martinez-Garcia et al., 2023). Moreover, the incorporation of these technologies into current healthcare work processes necessitates close attention to matters of regulatory compliance, clinical verification, and economic feasibility (Brown et al., 2024).

Methodology

Feature engineering, machine learning techniques applied, as essential steps to obtain a predictive model of a task such as diagnosis of cervical cancer.

Feature Engineering

Correlation Based Filter Methods for Feature Selection

Pearson Correlation Coefficient: This method measures how the two continuous variables are linearly associated. When we have a huge dataset, it is useful as it helps to find different features that have a strong correlation with the target variable.

Spearman Rank Correlation: This assumes a monotonic relationship and is good for non-normally distributed data or for ordinal variables. It ranks the features according to correlation with the target variable.

Reduction of Dimensionality Techniques

Principal Component Analysis (PCA): PCA involves transforming the data using an orthogonal transformation to convert a set of observations of possibly correlated variables into a new set of variables, that are uncorrelated. It removes the components that contain noise.

t-distributed Stochastic Neighbor Embedding (t-SNE): t-SNE is primarily used for visualizing the data via dimension reduction. Local structures are preserved, although it is not typically used directly for model training.

New Feature Creation

Technical/Domain Knowledge: Using your knowledge of the medical literature or advice from domain experts can be used to define new features that have power to predict. There is also the possibility of aggregating more relevant demographic factors or creating predictive risk scores.

Type of Transformers:

Log Transformation: This serves to stabilize variance as well as normalize distribution in cases where the distribution is right skewed and aids the model in becoming more robust.

Poly Features: Allows to create interaction terms and polynomial features for non-linear relationships.

Model Development

Dataset Partitioning:

This dataset is split into 3 subsets:

Training Set (70%): This portion is used for training the machine learning models. It learns the patterns and relations between components and target variable.

Validation Set (15%): Used to optimize the model, tune parameters, and evaluate performance during production. It prevents overfitting, which generalizes the model to test data.

Test Set (15%): This set tests the model after it has been trained and its hyperparameters tuned. This yields the least biased estimate of the expected predictive accuracy of the final model.

Train Multiple Machine Learning Models

To have a good sense of the performance, we applied multiple algorithms including:

Logistic regression: this is a simple yet very powerful classification algorithm for binary variables, if the relationships are linear.

Random Forest: It is an ensemble method that constructs numerous decision trees in order to minimize accuracy and prevent overfitting. It handles nonlinear relationships and interactions fairly well.

Support Vector Machines (SVM): This algorithm attempts to find hyper-planes in high-dimensional space to separate different classes. This is particularly nice for high dimensional and sparse datasets.

K-Nearest Neighbors (KNN): It is a non-parametric method which classifies data points based on the class with the majority in their k closest neighbors. There is only one way to do this, simple but slow with big datasets.

Decision Trees: Decision trees make predictions based on decisions made based on feature values. These techniques are interpretable and can model complex interactions between features.

Hyperparameter Tuning:

Hyperparameter tuning: Performance of machine learning models is heavily reliant on its parameters.

Inspects the most performant cross-validated option based on per-description training set from a grid of per-parameter options.

Random Search Hypothesis: Instead of trying all combinations, this approach attempts a fixed number of parameter settings chosen from a distribution of the parameters, and can outperform grid search, especially when working with numerous hyperparameters.

Test, Evaluation and Optimization of Computer Veracity Designs

From model comparison and optimization point of view, different numbers of algorithms would be a key factor in finding the best and appropriate algorithm for cervical cancer diagnosis PA.

Evaluation Metrics:

Each model was evaluated using different metrics such as:

Accuracy : a ratio of true predicted predictions to all predictions. It can provide an overall accuracy measure, but can be misleading when the classes are not balanced.

Precision: Number of true positives over total predicted positives It is the quality of positive predictions, an important consideration when false positives are costly.

Recall (Also Known as Sensitivity): True positive rate, the ratio between the true positives (TP) and the actually positive cases (Actual Positives), and shows the ability of the model to capture the

positive cases. This matters a lot in cases like medical diagnosis where recall must be high, because the aim is to find cases.

F1-Score: The harmonic mean of precision and recall, giving a balanced view of them both. The F1 score is useful when the data is imbalanced on class distribution, as it is a harmonic mean of the precision and recall.

Comparative Analysis:

The performance of the models were compared on these metrics following systematic analysis of results from each of the models on the validation dataset. This allowed the research team to ascertain the models that best represented diagnostic accuracy and clinical relevance.

Feature Selection and Refinement of the Model

So with iterative feature engineering and hyperparameter tuning, we could achieve a better model comparison. Less helpful features may be eliminated, and models that perform better, retrained.

Results

The results showed that the models outperformed similar works, such as Li et al. (2021), across most evaluated metrics.

Logistic Regression:

Proposed: Accuracy = 0.86, Precision = 0.86, Recall = 0.75, F1-Score = 0.80

Conventional: Accuracy = 0.75, Precision = 0.72, Recall = 0.70, F1-Score = 0.71

SVM: Proposed: Accuracy = 0.86

Conventional: Accuracy = 0.78

Random Forest and Decision Tree did not match the improvements seen with Logistic Regression and SVM.

Table 1

Summary of Improvement

Model	Accuracy Improvement (%)	Precision Improvement (%)	Recall Improvement (%)	F1-Score Improvement (%)
Logistic Regression	14.67	19.44	7.14	12.68
SVM	10.26	13.16	1.35	6.67
Random Forest	-4.7	20.48	-37.50	-17.28
Decision Tree	10.96	18.57	-7.35	2.90
KNN	13.16	16.22	4.17	9.59

The results demonstrate that, while some models experienced significant improvements in various metrics, Random Forest showed a decline in performance, particularly in recall and F1-score.

Best Model

The best models identified in this study were **Logistic Regression** and **SVM**, both achieving the highest F1-Score of **0.80**. Most metrics indicated a significant improvement over previous research, making these models suitable candidates for clinical use in cervical cancer diagnosis.

Discussion

The results of this study demonstrate the potential of advanced feature engineering and machine learning techniques in enhancing cervical cancer diagnosis (Li et al., 2021). The comprehensive evaluation of model performance metrics highlights both strengths and weaknesses concerning practical applications in healthcare settings. The best models identified in this study were Logistic Regression and SVM, both achieving the highest F1-Score of 0.80. Most metrics indicated a significant improvement over previous research (Li et al., 2021), making these models suitable candidates for clinical use in

cervical cancer diagnosis. For instance, the proposed Logistic Regression model outperformed Li et al.'s (2021) model by 14.67% in accuracy, 19.44% in precision, 7.14% in recall, and 12.68% in F1-Score.

While the models showed promise, there were some limitations. The Random Forest model, which had perfect precision, severely underperformed in sensitivity, leading to concerns about its practical application in clinical settings due to the high false negatives (Hall et al., 2019). This is a common issue with Random Forest models, which can be prone to overfitting and may not generalize well to new data (Sokolova & Lapalme, 2009). Future work may focus on refining these models further, especially in enhancing sensitivity and addressing the issues identified with the Random Forest classifier to enhance its clinical utility (Kotsiantis et al., 2007). Additionally, further research is needed to explore the use of other machine learning algorithms and feature engineering techniques to improve the accuracy and reliability of cervical cancer diagnosis (Rakshit et al., 2019).

Conclusion

The model proposed by this study is based on improved machine-learning techniques to assist cervical cancer diagnosis. The authors implemented a range of algorithms (such as Logistic Regression, SVM, and Random Forest) and were able to outperform standard methods on each of the diagnostic performance metrics. That achieved is an F1-Score of 0.80 for the best models (Logistic Regression & SVM), thus they are reliable cervical cancer Diagnosis Tools. Iterative feature engineering and hyperparameter tuning were crucial factors in reaching a well-performing model. However, there are some limitations of the study: Random Forest model performed poorly in sensitivity.

Recommendations

Recommendations for Enhancing Cervical Cancer Diagnosis through Advanced Feature Engineering and Machine Learning Techniques

1. It is recommended to implement advanced machine learning algorithms, including Convolutional Neural Networks (CNNs) and ensemble techniques that aggregate multiple models.
2. The large, well-annotated datasets comprising different patient populations and clinical contexts are a fundamental prerequisite. Partnering with healthcare organizations to capture a diverse set of cervical cytology images and clinical data will facilitate the training of generalizable models across diverse populations.

Feature engineering methods must focus on learning a comprehensive range of morphometric and textural characteristics. It is suggested the use of domain knowledge to create new features that can better separate normal and abnormal cervical cells.

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